Book 15681   Page   3   Project No. _____   Project Page

Exhibit R p.794 09/081,737

Investigator *Fang Chen* _____ Date

Subject *Final Assembling of UCP DNA Sequence*

Filed in Book Number/Title *Full Length cDNA Retrieving*

OIPE JC19
JUL 0 2 1999
PATENT & TRADEMARK OFFICE
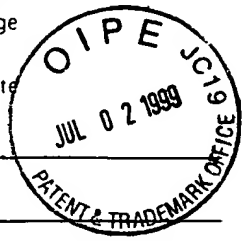
More sequence results were obtained from sequence
core facility. After a thorough editing, all the
DNA fragments assembled and contained open
reading frame coding for a protein with 58%
Identity to UCP1 and 73% to UCP2.
(See attached documents.)

contig_049)
Sequencher™ "nucr-est"

Diagram Key

Hole in contig	
Single fragment	
Multiple fragments same direction	
Both strands	
Both strands plus	

Start codon frame 1
Stop codon frame 2

Bumps on fragments show motifs, hollow rectangles show features

Page 1 of 2

for 9173

CompCheck: 1254

```
        Gap Weight:    3.000     Average Match:     0.540
     Length Weight:    0.100     Average Mismatch: -0.396

          Quality:   315.9           Length:       311
            Ratio:   1.032             Gaps:         2
Percent Similarity:  75.817   Percent Identity:  58.170
```

ucp3.pep x UCP1

```
  1 MVGLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQGENQAV 50
    |.||.:|||.||::|.:.::||.|||:||::||||||||||||:|||
  1 MGGLTASDVHPTLGVQLFSAGIAACLADVITFPLDTAKVRLQVQGE...C 47

 51 QTARLVQYRGVLGTILTMVRTEGPCSPYNGLVAGLQRQMSFASIRIGLYD 100
    .|..::.|:|||||||  .:|:|||. .  |.||.|||||||:| ||:|||||
 48 PTSSVIRYKGVLGTITAVVKTEGRMKLYSGLPAGLQRQISSASLRIGLYD 97

101 SVKQVYTPKGADNSSLTTRILAGCTTGAMAVTCAQPTDVVKVRFQASIHL 150
    .|.:..|:  ....||..:||||  |||:::.:||||:|||||:| ||
 98 TVQEFLTAGKETAPSLGSKILAGLTTGGVAVFIGQPTEVVKVRLQAQSHL 147

151 GPSRSDRKYSGTMDAYRTIAREEGVRGLWKGTLPNIMRNAIVNCAEVVTY 200
    . :.   :|.|| :|||.|| .|| |||||| ||:||..:||.|:|||
148 HGIKP..RYTGTYNAYRIIATTEGLTGLWKGTTPNLMRSVIINCTELVTY 195

201 DILKEKLLDYHLLTDNFPCHFVSAFGAGFCATVVASPVDVVKTRYMNSPP 250
    |::||  ::.  ::|.|:.|||:|||:  ||||||.:.||||||||||::|||
196 DLMKEAFVKNNILADDVPCHLVSALIAGFCATAMSSPVDVVKTRFINSPP 245

251 GQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLKRA 300
    ||| |. :| :|:...||||||:||:.||||||||||:|||.:|||||.
246 GQYKSVPNCAMKVFTNEGPTAFFKGLVPSFLRLGSWNVIMFVCFEQLKRE 295

301 LMKVQMLRESP 311
    || |.  .:::
296 LSKSRQTMDCA 306
```

CompCheck: 1254

Gap Weight: 3.000   Average Match: 0.540
Length Weight: 0.100   Average Mismatch: -0.396

Quality: 362.4   Length: 313
Ratio: 1.173   Gaps: 3
Percent Similarity: 85.065   Percent Identity: 73.377

ucp3.pep x UCP2

```
  1 MVGLKPSDVPPTMAVKFLGAGTAACFADLVTFPLDTAKVRLQIQGENQA. 49
    |||:|:.||||| .|||||||||||:|||:||||||||||||||||.|:
  1 MVGFKATDVPPTATVKFLGAGTAACIADLITFPLDTAKVRLQIQGESQGP 50

 50 VQTARLVQYRGVLGTILTMVRTEGPCSPYNGLVAGLQRQMSFASIRIGLY 99
    |... .|||||:||||||||||| | |||||||||||||||:|||||
 51 VRATASAQYRGVMGTILTMVRTEGPRSLYNGLVAGLQRQMSFASVRIGLY 100

100 DSVKQVYTPKGADNSSLTTRILAGCTTGAMAVTCAQPTDVVKVRFQASIH 149
    |||||.|| ||.:::.|:..|:|||:||||..|||||||||||||
101 DSVKQFYT.KGSEHASIGSRLLAGSTTGALAVAVAQPTDVVKVRFQAQAR 149

150 LGPSRSDRKYSGTMDAYRTIAREEGVRGLWKGTLPNIMRNAIVNCAEVVT 199
    |    ::|:| :|:::||:|||||||.|||||| ||: |||||||||:||
150 AG...GGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNCAELVT 196

200 YDILKEKLLDYHLLTDNFPCHFVSAFGAGFCATVVASPVDVVKTRYMNSP 249
    ||::|: ||. :|:||::||||:|||||||.||:||||||||||||||:
197 YDLIKDALLKANLMTDDLPCHFISAFGAGFCTTVIASPVDVVKTRYMNSA 246

250 PGQYFSPLDCMIKMVAQEGPTAFYKGFTPSFLRLGSWNVVMFVTYEQLKR 299
    ||| |: .| :.|:..||| ||||| |||||||||||||||||||||||
247 LGQYSSAGHCALTMLQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKR 296

300 ALMKVQMLRESPF 312
    ||| . ||.||
297 ALMAACTSREAPF 309
```